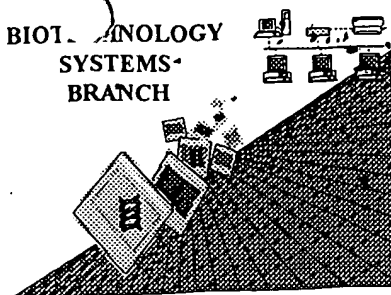


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/787228A
Source: O I P E
Date Processed by STIC: 9/10/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

DATE: 09/10/2001

PATENT APPLICATION: US/09/787,228A

TIME: 08:32:51

Input Set : A:\P198301.app

Output Set: N:\CRF3\09102001\I787228A.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Hine, Anna Victoria
 4 Morgan, Jane Leonie
 5 Santos, Albert Francis
 6 Palfrey, David
 8 <120> TITLE OF INVENTION: Gene and Protein Libraries and Methods Relating Thereto
 10 <130> FILE REFERENCE: PL9830
 12 <140> CURRENT APPLICATION NUMBER: 09/787,228A
 13 <141> CURRENT FILING DATE: 2001-03-14
 15 <150> PRIOR APPLICATION NUMBER: PCT/GB99/03081
 16 <151> PRIOR FILING DATE: 1999-09-14
 18 <150> PRIOR APPLICATION NUMBER: 98307434.5 EP
 19 <151> PRIOR FILING DATE: 1998-09-14
 21 <160> NUMBER OF SEQ ID NOS: 2
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 28
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
 32 peptide
 34 <400> SEQUENCE: 1
 35 Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser
 36 1 5 10 15
 38 Lys Lys Ser His Leu Val Ala His Gln Arg Thr His
 39 20 25
 42 <210> SEQ ID NO: 2
 43 <211> LENGTH: 28
 44 <212> TYPE: PRT
 45 <213> ORGANISM: Artificial Sequence ✓
 47 <220> FEATURE:
 48 <221> NAME/KEY: PEPTIDE
 49 <222> LOCATION: (17)
 50 <223> OTHER INFORMATION: Xaa is any amino acid
 52 <220> FEATURE:
 53 <221> NAME/KEY: PEPTIDE
 54 <222> LOCATION: (20)
 55 <223> OTHER INFORMATION: Xaa is any amino acid
 57 <220> FEATURE:
 58 <221> NAME/KEY: PEPTIDE
 59 <222> LOCATION: (23)
 60 <223> OTHER INFORMATION: Xaa is any amino acid
 62 <220> FEATURE:
 63 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
 64 peptide
 66 <400> SEQUENCE: 2
 67 Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser

Insufficient 223 response.
 An explanation of your
 artificial protein sequence
 is required in field 223

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

RAW SEQUENCE LISTING

DATE: 09/10/2001

PATENT APPLICATION: US/09/787,228A

TIME: 08:32:51

Input Set : A:\P198301.app

Output Set: N:\CRF3\09102001\I787228A.raw

68	1				5			10		15		
W--> 70	Xaa	Lys	Ser	Xaa	Leu	Val	Xaa	His	Gln	Arg	Thr	His
71				20				25				

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/787,228A

DATE: 09/10/2001

TIME: 08:32:52

Input Set : A:\P198301.app

Output Set: N:\CRF3\09102001\I787228A.raw

L:70 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/787 2284

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) all missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

SEQUENCE LISTING

<110> Hine, Anna Victoria
Morgan, Jane Leonie
Santos, Albert Francis
Palfrey, David

<120> Gene and Protein Libraries and Methods Relating Thereto

<130> PL9830

<140> 09/787,228

<141> 2001-03-14

<150> PCT/GB99/03081

<151> 1999-09-14

<150> 98307434.5 EP

<151> 1998-09-14

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
peptide

<400> 1

Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Pro	Glu	Cys	Gly	Lys	Ser	Phe	Ser
1				5				10					15		

Lys	Lys	Ser	His	Leu	Val	Ala	His	Gln	Arg	Thr	His
			20					25			

<210> 2

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (17)

<223> Xaa is any amino acid

<220>

<221> PEPTIDE

<222> (20)

<223> Xaa is any amino acid

<220>

<221> PEPTIDE

<222> (23)

<223> Xaa is any amino acid

<220>

<223> Description of Artificial Sequence: synthetic
peptide

<400> 2

Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Pro	Glu	Cys	Gly	Lys	Ser	Phe	Ser
1				5				10					15		

Xaa	Lys	Ser	Xaa	Leu	Val	Xaa	His	Gln	Arg	Thr	His
			20					25			